



1: AL050320. Human DNA sequenc...[gi:7263998]

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|------------|---|-----------|-----|--------|-----------------|
| LOCUS | HSJ1077I2 | 107057 bp | DNA | linear | PRI 25-OCT-2002 |
| DEFINITION | Human DNA sequence from clone RP5-1077I2 on chromosome 20 Contains the 3' end of the SPTLC2L gene for serine palmitoyltransferase long chain base subunit 2-like (aminotransferase 2), the 5' end of C20orf82 gene for a novel protein, part of 2 novel genes and a putative CpG island, complete sequence. | | | | |
| ACCESSION | AL050320 | | | | |
| VERSION | AL050320.19 GI:7263998 | | | | |
| KEYWORDS | HTG; aminotransferase; CpG island; serine palmitoyltransferase; SPTLC2L. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | <u>Homo sapiens</u> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| REFERENCE | 1 (bases 1 to 107057) | | | | |
| AUTHORS | Smith, M. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (22-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk | | | | |
| COMMENT | <p>On Mar 19, 2000 this sequence version replaced gi:6523711.</p> <p>During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.</p> <p>The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20</p> <p>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-1077I2 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm</p> <p>VECTOR: pCYPAC2</p> <p>----- Genome Center</p> <p>Center: Wellcome Trust Sanger Institute</p> <p>Center code: SC</p> <p>Web site: http://www.sanger.ac.uk</p> | | | | |

Contact: humquery@sanger.ac.uk

 IMPORTANT: This sequence is not the entire insert of clone RP5-1077I2. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP5-1077I2 is at 107057 in this sequence. The true right end of clone RP4-718P11 is at 100 in this sequence.

| FEATURES | Location/Qualifiers |
|----------------------|---|
| source | 1..107057 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="20" /clone="RP5-1077I2" /clone_lib="RPCI-5" |
| <u>repeat region</u> | complement(64..135) /note="L3b repeat: matches 1389..1462 of consensus" |
| <u>repeat region</u> | complement(164..264) /note="MIR repeat: matches 54..149 of consensus" |
| <u>repeat region</u> | complement(274..490) /note="L1PA4 repeat: matches 5942..6155 of consensus" |
| <u>repeat region</u> | 277..290 /note="4.7 copies 3 mer TTA 21% conserved" |
| gene | 730..844 /gene="SPTLC2L" |
| <u>mRNA</u> | <730..844 /gene="SPTLC2L" /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /note="continued from dJ718P11.1.1 in Em:AL109983 match: ESTs: Em:BQ011413" /evidence=not_experimental |
| <u>CDS</u> | <730..756 /gene="SPTLC2L" /note="continued from dJ718P11.1.1 in Em:AL109983" /codon_start=1 /evidence=not_experimental /product="dJ1077I2.2 (serine palmitoyltransferase, long chain base subunit 2-like (aminotransferase 2), variant 1)" /protein_id="CAD54807.1" /db_xref="GI:24412822" /db_xref="GOA:Q8IV87" /db_xref="SPTREMBL:Q8IV87" /translation="VICCVMKI" |
| <u>polyA signal</u> | 824..829 /gene="SPTLC2L" |
| <u>polyA site</u> | 844 /gene="SPTLC2L" |
| <u>repeat region</u> | 884..896 /note="2.6 copies 5 mer AAAAT 26% conserved" |
| <u>repeat region</u> | 992..1002 /note="2.2 copies 5 mer TTCTT 22% conserved" |
| <u>repeat region</u> | 1473..1494 /note="11.0 copies 2 mer AC 44% conserved" |
| <u>repeat region</u> | 1569..1580 /note="2.0 copies 6 mer CAAATG 24% conserved" |
| <u>repeat region</u> | 1871..1883 /note="2.2 copies 6 mer TTTTCC 26% conserved" |
| <u>repeat region</u> | complement(2399..2464) /note="MER5A repeat: matches 41..105 of consensus" |
| <u>misc feature</u> | 2513..2619 /note="match: STS: Em:Z94369" |

repeat region 2665..2674
 /note="2.5 copies 4 mer GATG 20% conserved"
repeat region 3122..3136
 /note="3.8 copies 4 mer TCTT 21% conserved"
repeat region 3368..3378
 /note="2.2 copies 5 mer ACAA 22% conserved"
repeat region 3615..3649
 /note="2.7 copies 13 mer TTCATGATTTTAA 70% conserved"
repeat region 3833..3848
 /note="8.0 copies 2 mer CA 23% conserved"
repeat region 3889..3898
 /note="2.5 copies 4 mer TGGT 20% conserved"
repeat region 4108..4247
 /note="MER5A repeat: matches 44..184 of consensus"
repeat region 4367..4377
 /note="2.2 copies 5 mer CTTCT 22% conserved"
misc feature complement(4488..5147)
 /note="match: GSS: Em:AQ262066"
repeat region 4535..4556
 /note="5.5 copies 4 mer TCTT 35% conserved"
repeat region complement(4541..4855)
 /note="AluSp repeat: matches 1..313 of consensus"
repeat region 4554..4570
 /note="17.0 copies 1 mer T 34% conserved"
repeat region 4637..4648
 /note="2.0 copies 6 mer ACCTCC 24% conserved"
repeat region 5056..5066
 /note="3.7 copies 3 mer GAT 22% conserved"
repeat region 5325..5364
 /note="20.0 copies 2 mer TG 44% conserved"
repeat region 5450..5460
 /note="2.8 copies 4 mer AAAT 22% conserved"
repeat region complement(5498..5566)
 /note="LTR16A repeat: matches 382..444 of consensus"
repeat region complement(5567..5760)
 /note="MER63A repeat: matches 1..209 of consensus"
repeat region complement(5761..6016)
 /note="LTR16A repeat: matches 95..382 of consensus"
repeat region complement(6066..6288)
 /note="L1MC5 repeat: matches 7695..7923 of consensus"
misc feature 7638..8163
 /note="match: GSS: Em:B52469"
repeat region 8095..8512
 /note="HAL1 repeat: matches 827..1248 of consensus"
repeat region 8095..8108
 /note="2.3 copies 6 mer AATAGA 28% conserved"
repeat region 8328..8341
 /note="2.0 copies 7 mer TAAAAAT 28% conserved"
repeat region complement(8732..8854)
 /note="L1ME repeat: matches 5436..5565 of consensus"
repeat region 8803..8817
 /note="5.0 copies 3 mer TAT 21% conserved"
repeat region 8892..8902
 /note="5.5 copies 2 mer AT 22% conserved"
repeat region 8970..9267
 /note="HAL1 repeat: matches 1507..1818 of consensus"
repeat region complement(9338..9408)
 /note="MLT1J2 repeat: matches 252..323 of consensus"
repeat region 10186..10197
 /note="2.0 copies 6 mer TTTCAC 24% conserved"
repeat region 10789..11086
 /note="AluJb repeat: matches 1..297 of consensus"
repeat region 11073..11086
 /note="14.0 copies 1 mer A 28% conserved"
repeat region 11170..11523

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| <u>repeat region</u> | /note="THE1B repeat: matches 1..364 of consensus" 11576..11800 |
| <u>repeat region</u> | /note="L1MED repeat: matches 2..249 of consensus" 11887..12242 |
| <u>misc feature</u> | /note="L1MED repeat: matches 363..751 of consensus" complement(11947..12544) |
| <u>repeat region</u> | /note="match: STS: Em:AL110056" 12237..12248 |
| <u>repeat region</u> | /note="2.0 copies 6 mer AGTAGA 24% conserved" 12365..12537 |
| <u>repeat region</u> | /note="L1MED repeat: matches 904..1084 of consensus" complement(12529..13073) |
| <u>repeat region</u> | /note="L1MA5A repeat: matches 3652..4242 of consensus" 13076..13330 |
| <u>repeat region</u> | /note="L1MA5A repeat: matches 4230..4483 of consensus" 13331..13638 |
| <u>repeat region</u> | /note="AluSx repeat: matches 1..307 of consensus" 13614..13629 |
| <u>repeat region</u> | /note="16.0 copies 1 mer A 23% conserved" 13639..15441 |
| <u>repeat region</u> | /note="L1MA5A repeat: matches 4483..6294 of consensus" 14424..14447 |
| <u>repeat region</u> | /note="8.0 copies 3 mer CAA 39% conserved" 14490..14500 |
| <u>repeat region</u> | /note="2.8 copies 4 mer ACAT 22% conserved" 15063..15077 |
| <u>repeat region</u> | /note="15.0 copies 1 mer A 30% conserved" 15091..15105 |
| <u>repeat region</u> | /note="2.1 copies 7 mer AAGTAAA 30% conserved" 15169..15208 |
| <u>repeat region</u> | /note="2.2 copies 18 mer GATACAAAATTACAGCTA 80% conserved" 15256..15266 |
| <u>repeat region</u> | /note="3.7 copies 3 mer TAA 22% conserved" 15437..15453 |
| <u>repeat region</u> | /note="2.8 copies 6 mer AAAAAT 25% conserved" 15775..15813 |
| <u>repeat region</u> | /note="19.5 copies 2 mer TG 69% conserved" 16015..16037 |
| <u>misc feature</u> | /note="1.9 copies 12 mer TGAGAGGCCTCT 37% conserved" complement(16370..16537) |
| <u>repeat region</u> | /note="match: GSS: Em:AQ044245" 16866..16878 |
| <u>repeat region</u> | /note="2.6 copies 5 mer TTCCC 26% conserved" 17442..17817 |
| <u>repeat region</u> | /note="LTR16C repeat: matches 85..489 of consensus" 17825..17836 |
| <u>repeat region</u> | /note="2.4 copies 5 mer TCTTT 24% conserved" 18048..18267 |
| <u>misc feature</u> | /note="MIR repeat: matches 12..247 of consensus" 18343..18706 |
| <u>repeat region</u> | /note="match: GSS: Em:AQ099012" 18517..18616 |
| <u>repeat region</u> | /note="L2 repeat: matches 2932..3031 of consensus" 18534..18544 |
| <u>repeat region</u> | /note="3.7 copies 3 mer TTC 22% conserved" 18699..18714 |
| <u>repeat region</u> | /note="3.2 copies 5 mer TGCAT 23% conserved" 19041..19141 |
| <u>repeat region</u> | /note="L2 repeat: matches 3199..3312 of consensus" 19147..19156 |
| <u>repeat region</u> | /note="2.5 copies 4 mer AAAT 20% conserved" 19309..19810 |
| <u>repeat region</u> | /note="MLT1H repeat: matches 19..549 of consensus" 19673..19682 |
| | /note="2.5 copies 4 mer CCAT 20% conserved" |

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| <u>repeat region</u> | 20051..20064 /note="2.0 copies 7 mer AACAAATG 28% conserved" |
| <u>repeat region</u> | 20123..20430 /note="AluY repeat: matches 3..310 of consensus" |
| <u>repeat region</u> | 20402..20418 /note="17.0 copies 1 mer A 34% conserved" |
| <u>repeat region</u> | 20416..20431 /note="4.0 copies 4 mer AAAG 32% conserved" |
| <u>repeat region</u> | 20437..20454 /note="2.2 copies 8 mer TAGTGTGG 36% conserved" |
| <u>repeat region</u> | complement(20475..20589) /note="L2 repeat: matches 3197..3310 of consensus" |
| <u>repeat region</u> | 20658..20667 /note="3.3 copies 3 mer ATG 20% conserved" |
| <u>repeat region</u> | 20704..20714 /note="2.2 copies 5 mer ATTGT 22% conserved" |
| <u>repeat region</u> | 20893..20904 /note="2.0 copies 6 mer TCACAA 24% conserved" |
| <u>repeat region</u> | 21003..21054 /note="MLT1H repeat: matches 107..157 of consensus" |
| <u>repeat region</u> | 21187..21290 /note="MLT1F repeat: matches 414..503 of consensus" |
| <u>repeat region</u> | 21404..21570 /note="L1MC/D repeat: matches 5265..5449 of consensus" |
| <u>repeat region</u> | 21450..21460 /note="2.8 copies 4 mer AATA 22% conserved" |
| <u>repeat region</u> | 22192..22765 /note="L1MCc repeat: matches -514..418 of consensus" |
| <u>repeat region</u> | 22348..22368 /note="2.1 copies 10 mer GGGCATCCAG 42% conserved" |
| <u>repeat region</u> | 22595..22606 /note="2.0 copies 6 mer CTGGCT 24% conserved" |
| <u>repeat region</u> | 22884..23840 /note="L1MCc repeat: matches 435..1471 of consensus" |
| <u>repeat region</u> | 23773..23786 /note="4.7 copies 3 mer AAC 28% conserved" |
| <u>repeat region</u> | 23789..23798 /note="10.0 copies 1 mer A 20% conserved" |
| <u>repeat region</u> | 23841..24130 /note="AluSc repeat: matches 1..304 of consensus" |
| <u>repeat region</u> | 24106..24130 /note="25.0 copies 1 mer A 50% conserved" |
| <u>repeat region</u> | 24131..24246 /note="L1MCc repeat: matches 1471..1579 of consensus" |
| <u>repeat region</u> | 24187..24198 /note="2.0 copies 6 mer AAGGAT 24% conserved" |
| <u>repeat region</u> | 24247..24456 /note="MSTD repeat: matches 1..213 of consensus" |
| <u>repeat region</u> | 24309..24327 /note="9.5 copies 2 mer TA 29% conserved" |
| <u>repeat region</u> | 24461..25134 /note="L1MA5 repeat: matches 4023..4699 of consensus" |
| <u>repeat region</u> | 24510..24519 /note="3.3 copies 3 mer AAG 20% conserved" |
| <u>repeat region</u> | 24696..24706 /note="2.8 copies 4 mer AATA 22% conserved" |
| <u>repeat region</u> | 25135..25562 /note="MER57B repeat: matches 1..434 of consensus" |
| <u>repeat region</u> | 25563..26664 /note="L1PA17 repeat: matches 5026..6150 of consensus" |
| <u>repeat region</u> | 25642..25656 /note="2.5 copies 6 mer CAAAAG 21% conserved" |
| <u>repeat region</u> | 25957..25967 /note="2.2 copies 5 mer CAAAA 22% conserved" |
| <u>repeat region</u> | 26656..26667 |

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| <u>repeat region</u> | /note="2.4 copies 5 mer AAAAG 24% conserved" 26665..28260 |
| <u>repeat region</u> | /note="L1MA5 repeat: matches 4697..6294 of consensus" 27145..27155 |
| <u>repeat region</u> | /note="2.8 copies 4 mer AACC 22% conserved" 27321..27335 |
| <u>repeat region</u> | /note="15.0 copies 1 mer A 21% conserved" 27537..27547 |
| <u>repeat region</u> | /note="2.2 copies 5 mer AAAAC 22% conserved" 27622..27634 |
| <u>repeat region</u> | /note="2.6 copies 5 mer AAAGG 26% conserved" 27794..27809 |
| <u>repeat region</u> | /note="2.0 copies 8 mer ATTTCTGC 25% conserved" 27920..27937 |
| <u>repeat region</u> | /note="3.0 copies 6 mer TAGAAG 27% conserved" 27966..27978 |
| <u>repeat region</u> | /note="2.6 copies 5 mer AGAGG 26% conserved" 28103..28112 |
| <u>repeat region</u> | /note="2.5 copies 4 mer AAGA 20% conserved" 28280..28413 |
| <u>repeat region</u> | /note="MSTD repeat: matches 249..388 of consensus" 28416..28624 |
| <u>repeat region</u> | /note="L1MCc repeat: matches 1692..1885 of consensus" 28628..28911 |
| <u>repeat region</u> | /note="AluJo repeat: matches 1..286 of consensus" 28911..28931 |
| <u>repeat region</u> | /note="10.5 copies 2 mer AC 33% conserved" complement(28955..29226) |
| <u>repeat region</u> | /note="AluJo repeat: matches 1..252 of consensus" 29016..29026 |
| <u>repeat region</u> | /note="2.2 copies 5 mer CTCAC 22% conserved" 29094..29116 |
| <u>repeat region</u> | /note="23.0 copies 1 mer T 28% conserved" 29245..29262 |
| <u>repeat region</u> | /note="2.0 copies 9 mer AAGTAACAA 36% conserved" 29273..29694 |
| <u>repeat region</u> | /note="L1MCc repeat: matches 2043..2479 of consensus" 29535..29569 |
| <u>repeat region</u> | /note="4.4 copies 8 mer AAAAAAGC 25% conserved" complement(29928..30344) |
| <u>repeat region</u> | /note="MLT1L repeat: matches 110..609 of consensus" 30011..30031 |
| <u>repeat region</u> | /note="1.9 copies 11 mer AGAGAAAGGCC 33% conserved" complement(30285..30361) |
| <u>repeat region</u> | /note="LTR67 repeat: matches 97..174 of consensus" 30917..30967 |
| <u>repeat region</u> | /note="25.5 copies 2 mer TG 93% conserved" 31093..31109 |
| <u>repeat region</u> | /note="2.1 copies 8 mer AAAGAGAT 34% conserved" complement(31180..31295) |
| <u>repeat region</u> | /note="MLT1K repeat: matches 111..228 of consensus" 31292..31305 |
| <u>repeat region</u> | /note="2.0 copies 7 mer TAAAATG 28% conserved" 31429..31438 |
| <u>repeat region</u> | /note="3.3 copies 3 mer. TTC 20% conserved" 31509..31556 |
| <u>repeat region</u> | /note="MADE1 repeat: matches 33..80 of consensus" 31669..32100 |
| <u>repeat region</u> | /note="LTR16C repeat: matches 38..491 of consensus" 31776..31786 |
| <u>repeat region</u> | /note="2.2 copies 5 mer AAGTC 22% conserved" 31901..31914 |
| <u>repeat region</u> | /note="2.0 copies 7 mer TCACAGA 28% conserved" 32165..32175 |
| <u>repeat region</u> | /note="2.2 copies 5 mer ATTTT 22% conserved" |

repeat region 32453..32470
/note="3.6 copies 5 mer AAAGA 27% conserved"

repeat region 32571..32606
/note="2.1 copies 17 mer CAAGCTAGTAACTAAC 54% conserved"

repeat region 32790..32873
/note="L2 repeat: matches 2922..3014 of consensus"

repeat region 32897..32955
/note="Charlie5 repeat: matches 1..59 of consensus"

repeat region 33143..33152
/note="2.5 copies 4 mer ATAC 20% conserved"

repeat region 33916..33929
/note="2.0 copies 7 mer TTCCTC 28% conserved"

repeat region 34580..34591
/note="3.0 copies 4 mer ATAA 24% conserved"

repeat region complement(34609..34923)
/note="MLT1A repeat: matches 1..316 of consensus"

repeat region complement(34924..34993)
/note="L1MB1 repeat: matches 6082..6152 of consensus"

repeat region 34968..34978
/note="2.2 copies 5 mer ACAAT 22% conserved"

repeat region 34989..34999
/note="2.2 copies 5 mer AGGCA 22% conserved"

repeat region 35137..35170
/note="5.7 copies 6 mer TTTTTC 34% conserved"

repeat region 35150..35251
/note="25.5 copies 4 mer TTTC 150% conserved"

repeat region 35229..35286
/note="14.5 copies 4 mer TTCC 98% conserved"

repeat region complement(35285..35575)
/note="AluJo repeat: matches 1..294 of consensus"

repeat region 35447..35458
/note="12.0 copies 1 mer T 24% conserved"

repeat region 35588..35606
/note="3.8 copies 5 mer TTTTG 31% conserved"

repeat region 35654..35665
/note="2.0 copies 6 mer CTTATT 24% conserved"

repeat region 35729..35764
/note="2.4 copies 15 mer CCTTCCTTTCTCCCT 63% conserved"

repeat region 35767..35783
/note="4.2 copies 4 mer CCTC 25% conserved"

repeat region complement(35820..35892)
/note="L2 repeat: matches 3170..3243 of consensus"

repeat region 36014..36031
/note="3.0 copies 6 mer TATTTA 27% conserved"

repeat region 36866..36882
/note="8.5 copies 2 mer TC 34% conserved"

repeat region 37023..37077
/note="3.7 copies 15 mer AAAATGAAATAAAAC 67% conserved"

repeat region complement(37215..37423)
/note="MIR repeat: matches 31..261 of consensus"

repeat region 37273..37283
/note="2.8 copies 4 mer ATTA 22% conserved"

repeat region complement(37520..37798)
/note="L2 repeat: matches 2456..2742 of consensus"

repeat region 37766..37784
/note="3.8 copies 5 mer GGAGG 29% conserved"

repeat region 37896..37906
/note="2.8 copies 4 mer AAAG 22% conserved"

repeat region 37954..37965
/note="12.0 copies 1 mer A 24% conserved"

repeat region complement(38128..38424)
/note="AluSg repeat: matches 2..297 of consensus"

repeat region 38128..38144
/note="17.0 copies 1 mer T 34% conserved"

repeat region 38492..38911

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| <u>repeat region</u> | /note="MER63B repeat: matches 1..435 of consensus" 38494..38504 |
| <u>repeat region</u> | /note="2.2 copies 5 mer GTGAT 22% conserved" complement(38945..39370) |
| <u>repeat region</u> | /note="MER57A repeat: matches 1..403 of consensus" 38967..38976 |
| <u>repeat region</u> | /note="2.0 copies 5 mer AAATT 20% conserved" complement(39472..39532) |
| <u>repeat region</u> | /note="L2 repeat: matches 3205..3262 of consensus" complement(39534..39674) |
| <u>repeat region</u> | /note="MIR repeat: matches 108..259 of consensus" 39631..39640 |
| <u>repeat region</u> | /note="3.3 copies 3 mer TAT 20% conserved" 39720..39729 |
| <u>repeat region</u> | /note="2.5 copies 4 mer ATAA 20% conserved" 39931..39964 |
| <u>repeat region</u> | /note="2.1 copies 16 mer ATGGATAAATAAATTA 59% conserved" 39935..39944 |
| <u>repeat region</u> | /note="2.5 copies 4 mer ATAA 20% conserved" 39954..39967 |
| <u>misc feature</u> | /note="3.5 copies 4 mer AATT 28% conserved" 40707..41300 |
| <u>repeat region</u> | /note="match: GSS: Em:AG040344" 40893..40925 |
| <u>repeat region</u> | /note="16.5 copies 2 mer TA 41% conserved" complement(40925..41068) |
| <u>repeat region</u> | /note="AluSg/x repeat: matches 145..288 of consensus" 41444..41755 |
| <u>repeat region</u> | /note="L2 repeat: matches 2697..3050 of consensus" complement(41764..42122) |
| <u>repeat region</u> | /note="MLT1A repeat: matches 21..365 of consensus" 41860..41871 |
| <u>repeat region</u> | /note="2.0 copies 6 mer TCAAGA 24% conserved" complement(42157..42433) |
| <u>repeat region</u> | /note="LTR16C repeat: matches 88..391 of consensus" 42162..42175 |
| <u>repeat region</u> | /note="2.3 copies 6 mer AGTGAG 28% conserved" 42759..42771 |
| <u>repeat region</u> | /note="2.2 copies 6 mer ATTTTA 26% conserved" complement(42785..42863) |
| <u>repeat region</u> | /note="MLT1J2 repeat: matches 368..448 of consensus" 42864..42880 |
| <u>repeat region</u> | /note="2.1 copies 8 mer AAAATAAT 34% conserved" 42866..42885 |
| <u>repeat region</u> | /note="6.7 copies 3 mer AAT 24% conserved" complement(42894..43239) |
| <u>repeat region</u> | /note="MLT1J2 repeat: matches 23..386 of consensus" 43074..43099 |
| <u>repeat region</u> | /note="6.5 copies 4 mer AGAA 25% conserved" 43258..43274 |
| <u>repeat region</u> | /note="2.4 copies 7 mer AAATTAG 25% conserved" complement(43270..43331) |
| <u>repeat region</u> | /note="MER113 repeat: matches 32..95 of consensus" 43285..43294 |
| <u>misc feature</u> | /note="3.3 copies 3 mer TAA 20% conserved" 43413..43703 |
| <u>repeat region</u> | /note="match: GSS: Em:AQ015991" complement(43476..43514) |
| <u>repeat region</u> | /note="MLT1H repeat: matches 538..577 of consensus" complement(43521..43739) |
| <u>repeat region</u> | /note="MLT1H repeat: matches 133..375 of consensus" 43708..43724 |
| <u>repeat region</u> | /note="2.4 copies 7 mer CCACAAG 25% conserved" complement(43740..44231) |
| <u>repeat region</u> | /note="MLT2B2 repeat: matches 1..515 of consensus" |

repeat region 43777..43811
/note="3.5 copies 10 mer AGACATAGAT 34% conserved"

repeat region 43787..43799
/note="3.2 copies 4 mer ATAG 26% conserved"

repeat region 43805..43829
/note="4.2 copies 6 mer ACAGAC 41% conserved"

repeat region 44002..44012
/note="2.8 copies 4 mer TCAA 22% conserved"

repeat region 44352..44361
/note="10.0 copies 1 mer A 20% conserved"

misc feature complement(44542..44977)
/note="match: GSS: Em:AQ358298"

repeat region 44830..45320
/note="MLT1H repeat: matches 1..549 of consensus"

repeat region 45523..45540
/note="2.2 copies 8 mer AAACATGA 27% conserved"

repeat region 45570..45674
/note="MLT1J2 repeat: matches 325..428 of consensus"

repeat region 45791..45806
/note="2.3 copies 7 mer ATTGATT 23% conserved"

misc feature 45853..46320
/note="match: GSS: Em:AQ186434"

repeat region complement(46233..46722)
/note="L1ME3 repeat: matches 5657..6158 of consensus"

repeat region 46777..46875
/note="L1ME3A repeat: matches 5743..5846 of consensus"

repeat region 46990..47021
/note="16.0 copies 2 mer GT 64% conserved"

repeat region 47140..47154
/note="5.0 copies 3 mer ATA 21% conserved"

repeat region 47427..47443
/note="2.4 copies 7 mer AGGAGAA 25% conserved"

repeat region 48160..48233
/note="MER58 repeat: matches 25..98 of consensus"

repeat region 48223..48253
/note="2.1 copies 15 mer TTTTAAATGGTCATA 44% conserved"

repeat region 48247..48348
/note="MER58 repeat: matches 2318..2417 of consensus"

repeat region 48457..48560
/note="MLT1J2 repeat: matches 32..133 of consensus"

repeat region 48655..48816
/note="MLT1J2 repeat: matches 288..450 of consensus"

repeat region 48880..48894
/note="7.5 copies 2 mer AC 30% conserved"

repeat region 50127..50602
/note="L1MC4 repeat: matches 7392..7858 of consensus"

repeat region 50173..50182
/note="2.0 copies 5 mer AACAT 20% conserved"

repeat region 50243..50255
/note="2.2 copies 6 mer ATACAA 26% conserved"

repeat region 50380..50393
/note="2.3 copies 6 mer ATGACA 28% conserved"

repeat region complement(50622..50888)
/note="MLT1H repeat: matches 224..531 of consensus"

repeat region 50893..50936
/note="22.0 copies 2 mer CA 88% conserved"

repeat region 50936..50998
/note="31.5 copies 2 mer AG 72% conserved"

repeat region complement(50977..51089)
/note="MLT1H repeat: matches 90..231 of consensus"

repeat region 51256..51413
/note="L1ME3A repeat: matches 5876..6065 of consensus"

repeat region 51508..51657
/note="MIR3 repeat: matches 23..179 of consensus"

repeat region complement(52443..52527)

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|----------------------|---|
| <u>repeat region</u> | /note="L2 repeat: matches 3204..3312 of consensus" 52443..52452 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TTCA 20% conserved" complement(52602..52691) |
| <u>repeat region</u> | /note="MIR repeat: matches 101..187 of consensus" 52649..52666 |
| <u>repeat region</u> | /note="2.0 copies 9 mer CAGACGAGG 27% conserved" 52772..52984 |
| <u>repeat region</u> | /note="MER58A repeat: matches 1..223 of consensus" complement(53007..53400) |
| <u>repeat region</u> | /note="MLT1J2 repeat: matches 1..445 of consensus" 53222..53232 |
| <u>repeat region</u> | /note="2.2 copies 5 mer AAAAG 22% conserved" 53515..53738 |
| <u>repeat region</u> | /note="L1MC5 repeat: matches 7701..7928 of consensus" 53789..53812 |
| <u>repeat region</u> | /note="4.8 copies 5 mer AAAAT 32% conserved" complement(54168..54323) |
| <u>repeat region</u> | /note="MLT1J2 repeat: matches 267..434 of consensus" 54341..54661 |
| <u>repeat region</u> | /note="AluSx repeat: matches 1..312 of consensus" 54620..54632 |
| <u>repeat region</u> | /note="13.0 copies 1 mer A 26% conserved" 54633..54647 |
| <u>repeat region</u> | /note="3.8 copies 4 mer GAAT 30% conserved" 54646..54661 |
| <u>repeat region</u> | /note="16.0 copies 1 mer A 23% conserved" 55244..55258 |
| <u>repeat region</u> | /note="3.8 copies 4 mer ATTC 21% conserved" 55249..55270 |
| <u>repeat region</u> | /note="1.8 copies 12 mer TTCATACATTTG 37% conserved" 55694..55705 |
| <u>repeat region</u> | /note="2.0 copies 6 mer CCCTTT 24% conserved" 56046..56055 |
| <u>repeat region</u> | /note="2.5 copies 4 mer AGTT 20% conserved" 56363..56373 |
| <u>repeat region</u> | /note="2.8 copies 4 mer TTAT 22% conserved" 56397..58342 |
| <u>misc feature</u> | /note="CpG island" /evidence=not_experimental |
| <u>repeat region</u> | 56508..56526 |
| <u>repeat region</u> | /note="3.8 copies 5 mer GGGCT 20% conserved" 57013..57027 |
| <u>repeat region</u> | /note="3.0 copies 5 mer CTCCC 21% conserved" 57209..57220 |
| <u>repeat region</u> | /note="2.0 copies 6 mer CTCCAG 24% conserved" 57255..57269 |
| <u>repeat region</u> | /note="3.0 copies 5 mer CCACC 23% conserved" 57259..57271 |
| <u>repeat region</u> | /note="3.2 copies 4 mer CCCA 26% conserved" 57458..57472 |
| <u>repeat region</u> | /note="3.0 copies 5 mer GCGGC 21% conserved" 57534..57549 |
| <u>repeat region</u> | /note="2.7 copies 6 mer GGCGAG 23% conserved" 57541..57654 |
| <u>misc feature</u> | /note="Single clone region. single clone region containing only reads from a Short insert library of 20bae55h7. Assembly consistant with digest." |
| <u>repeat region</u> | 57586..57659 |
| <u>repeat region</u> | /note="24.7 copies 3 mer CCT 121% conserved" 57677..57689 |
| <u>repeat region</u> | /note="2.2 copies 6 mer CCGCTC 26% conserved" 57699..58288 |
| <u>repeat region</u> | /note="L1M2 repeat: matches 661..1268 of consensus" 57748..57769 |

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| <u>repeat region</u> | /note="4.4 copies 5 mer CCCGC 26% conserved" 57749..57762 |
| <u>repeat region</u> | /note="4.7 copies 3 mer CCG 21% conserved" 57794..57807 |
| <u>repeat region</u> | /note="2.8 copies 5 mer CCGGC 28% conserved" 57831..57843 |
| <u>repeat region</u> | /note="2.2 copies 6 mer GTCTCC 26% conserved" 57841..57857 |
| <u>repeat region</u> | /note="5.7 copies 3 mer CCG 34% conserved" 57926..57954 |
| <u>repeat region</u> | /note="9.7 copies 3 mer GCG 49% conserved" 58021..58050 |
| <u>repeat region</u> | /note="2.5 copies 12 mer GGAGCCCAGGCG 42% conserved" 58057..58073 |
| <u>repeat region</u> | /note="2.1 copies 8 mer CCGGGCTC 34% conserved" 58070..58085 |
| <u>repeat region</u> | /note="5.3 copies 3 mer CTC 23% conserved" 58096..58122 |
| <u>repeat region</u> | /note="9.0 copies 3 mer CCG 38% conserved" 58098..58122 |
| <u>repeat region</u> | /note="3.6 copies 7 mer GCCGCCG 34% conserved" 58170..58199 |
| <u>repeat region</u> | /note="10.0 copies 3 mer GCT 42% conserved" 58238..58257 |
| <u>repeat region</u> | /note="2.0 copies 10 mer CCGACGCGGC 33% conserved" 58518..58527 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TCTG 20% conserved" 58603..58612 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TGCT 20% conserved" 58836..58847 |
| <u>repeat region</u> | /note="2.0 copies 6 mer TTCCTC 24% conserved" 59256..59559 |
| <u>repeat region</u> | /note="AluSx repeat: matches 3..312 of consensus" 59530..59564 |
| <u>repeat region</u> | /note="35.0 copies 1 mer A 25% conserved" 59531..59593 |
| <u>repeat region</u> | /note="12.6 copies 5 mer AAAAT 80% conserved" 59646..59664 |
| <u>repeat region</u> | /note="1.9 copies 10 mer CTTTATACAT 29% conserved" complement(59700..59873) |
| <u>repeat region</u> | /note="MIR repeat: matches 82..260 of consensus" 60390..60614 |
| <u>misc feature</u> | /note="match: GSS: Em:AQ046228 match: STS: Em:G50471" 60507..60518 |
| <u>repeat region</u> | /note="2.0 copies 6 mer CAGCTT 24% conserved" 60828..60837 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TTCT 20% conserved" 61115..61124 |
| <u>repeat region</u> | /note="3.3 copies 3 mer AGT 20% conserved" complement(61136..61206) |
| <u>repeat region</u> | /note="MIR repeat: matches 193..262 of consensus" 61206..61217 |
| <u>repeat region</u> | /note="3.0 copies 4 mer CTTT 24% conserved" complement(61207..61525) |
| <u>repeat region</u> | /note="AluY repeat: matches 1..311 of consensus" 61215..61236 |
| <u>repeat region</u> | /note="22.0 copies 1 mer T 44% conserved" 61386..61399 |
| <u>repeat region</u> | /note="14.0 copies 1 mer T 28% conserved" complement(61526..61637) |
| <u>repeat region</u> | /note="MIR repeat: matches 77..193 of consensus" 61798..61812 |
| <u>repeat region</u> | /note="7.5 copies 2 mer AT 21% conserved" 62222..62233 |

repeat region /note="2.0 copies 6 mer TTAATG 24% conserved"
62245..62271

repeat region /note="4.5 copies 6 mer ATAGAT 45% conserved"
62788..62798

repeat region /note="11.0 copies 1 mer T 22% conserved"
complement(62812..63323)

repeat region /note="MLT1H repeat: matches 18..549 of consensus"
complement(63386..63567)

repeat region /note="L1M4 repeat: matches 2247..2434 of consensus"
complement(63587..63875)

repeat region /note="AluY repeat: matches 1..289 of consensus"
63591..64190

repeat region /note="15.0 copies 40 mer
TTTTGAGACGGAGTCTCACTCTATCACCCAGGCTGGAGTG 909% conserved"
complement(63880..64180)

repeat region /note="AluY repeat: matches 1..301 of consensus"
63880..63899

repeat region /note="20.0 copies 1 mer T 31% conserved"
64188..64197

repeat region /note="2.0 copies 5 mer TTAA 20% conserved"
64321..64331

repeat region /note="3.7 copies 3 mer GCT 22% conserved"
complement(64333..64645)

repeat region /note="AluSx repeat: matches 1..305 of consensus"
64333..64355

repeat region /note="23.0 copies 1 mer T 37% conserved"
64645..64658

repeat region /note="4.7 copies 3 mer CTG 28% conserved"
complement(64676..65154)

repeat region /note="HAL1 repeat: matches 1214..1726 of consensus"
64852..64861

repeat region /note="2.0 copies 5 mer AATTT 20% conserved"
65434..65470

repeat region /note="3.4 copies 11 mer CTTTTCTTTC 51% conserved"
65446..65528

repeat region /note="20.8 copies 4 mer CTTT 37% conserved"
65475..65487

repeat region /note="2.6 copies 5 mer TTCCT 26% conserved"
65505..65524

repeat region /note="10.0 copies 2 mer TC 33% conserved"
65532..65550

repeat region /note="1.9 copies 10 mer TTTTTTAAAG 38% conserved"
complement(65542..66060)

repeat region /note="L1ME2 repeat: matches 5634..6164 of consensus"
66207..66216

repeat region /note="5.0 copies 2 mer CT 20% conserved"
complement(66506..66872)

repeat region /note="L3b repeat: matches 1114..1476 of consensus"
66655..66673

repeat region /note="2.1 copies 9 mer TGTTCACTT 38% conserved"
66945..66955

repeat region /note="2.2 copies 5 mer AAAGA 22% conserved"
67043..67053

repeat region /note="2.2 copies 5 mer GATGG 22% conserved"
67091..67100

repeat region /note="2.5 copies 4 mer CAAA 20% conserved"
67118..67147

repeat region /note="6.0 copies 5 mer AGAAA 44% conserved"
67120..67148

repeat region /note="29.0 copies 1 mer A 31% conserved"
67189..67206

repeat region /note="2.0 copies 9 mer TTATAAGAA 36% conserved"
67235..67247

repeat region /note="3.2 copies 4 mer TTTC 26% conserved"
67311..67498

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| <u>repeat region</u> | /note="LTR16C repeat: matches 289..488 of consensus" 67609..67618 |
| <u>repeat region</u> | /note="3.3 copies 3 mer TTG 20% conserved" 68515..68525 |
| <u>repeat region</u> | /note="3.7 copies 3 mer TTA 22% conserved" complement(68524..68539) |
| <u>repeat region</u> | /note="L1MA10 repeat: matches 6319..6334 of consensus" complement(68540..69072) |
| <u>repeat region</u> | /note="L1ME1 repeat: matches 5582..6161 of consensus" 68776..68790 |
| <u>repeat region</u> | /note="3.0 copies 5 mer TGCAT 21% conserved" 68816..68825 |
| <u>repeat region</u> | /note="2.5 copies 4 mer ATTC 20% conserved" 69398..69414 |
| <u>repeat region</u> | /note="17.0 copies 1 mer A 25% conserved" 69473..69489 |
| <u>repeat region</u> | /note="1.9 copies 9 mer ATTCTCTTG 27% conserved" 69481..69508 |
| <u>repeat region</u> | /note="2.2 copies 13 mer ATTCTCTTGCCCC 40% conserved" 69688..69987 |
| <u>repeat region</u> | /note="AluSp repeat: matches 2..302 of consensus" 69969..69987 |
| <u>repeat region</u> | /note="19.0 copies 1 mer A 38% conserved" 70233..70333 |
| <u>repeat region</u> | /note="MER5A repeat: matches 9..112 of consensus" complement(70347..71285) |
| <u>repeat region</u> | /note="L1PB4 repeat: matches 5215..6152 of consensus" 70594..70605 |
| <u>repeat region</u> | /note="2.0 copies 6 mer TTTCTG 24% conserved" 71051..71065 |
| <u>repeat region</u> | /note="2.5 copies 6 mer TTTTAA 21% conserved" 71104..71128 |
| <u>repeat region</u> | /note="2.3 copies 11 mer TTGTTGTCCTC 32% conserved" 71286..71350 |
| <u>repeat region</u> | /note="MER5A repeat: matches 124..189 of consensus" 71430..71439 |
| <u>repeat region</u> | /note="3.3 copies 3 mer TAA 20% conserved" 71501..71516 |
| <u>repeat region</u> | /note="2.0 copies 8 mer CATGGGTC 32% conserved" complement(71650..71724) |
| <u>repeat region</u> | /note="MLT1I repeat: matches 104..180 of consensus" 71726..71873 |
| <u>repeat region</u> | /note="MIR repeat: matches 25..183 of consensus" 72208..72223 |
| <u>repeat region</u> | /note="4.0 copies 4 mer TTCC 23% conserved" complement(72301..72592) |
| <u>repeat region</u> | /note="AluSc repeat: matches 4..294 of consensus" 72301..72315 |
| <u>repeat region</u> | /note="15.0 copies 1 mer T 21% conserved" 72378..72389 |
| <u>repeat region</u> | /note="2.0 copies 6 mer ACCTCC 24% conserved" 72445..72454 |
| <u>repeat region</u> | /note="3.3 copies 3 mer CCA 20% conserved" complement(72715..72839) |
| <u>repeat region</u> | /note="THE1A repeat: matches 1..126 of consensus" complement(72840..73499) |
| <u>repeat region</u> | /note="THE1A-int repeat: matches 918..1580 of consensus" 72941..72960 |
| <u>repeat region</u> | /note="2.9 copies 7 mer AAAGTCC 31% conserved" 73481..73492 |
| <u>repeat region</u> | /note="2.0 copies 6 mer CCCTGC 24% conserved" complement(73505..73581) |
| <u>repeat region</u> | /note="THE1A repeat: matches 1..80 of consensus" 73583..74087 |
| <u>repeat region</u> | /note="L1ME3A repeat: matches 5610..6157 of consensus" |

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gene      complement(join(74174..74482,75357..75477,75826..76047))
          /gene="dJ1077I2.4"
mRNA      complement(join(74174..74482,75357..75477,75826..76047))
          /gene="dJ1077I2.4"
          /product="dJ1077I2.4 (Putative novel transcript)"
          /note="match: ESTs: Em:BI463885"
          /evidence=not_experimental
repeat region 74749..74764
              /note="2.0 copies 8 mer GGCAAAAT 32% conserved"
repeat region 75388..75401
              /note="2.0 copies 7 mer AGTGTGA 28% conserved"
repeat region 75754..75766
              /note="2.2 copies 6 mer TGGCCT 26% conserved"
repeat region 75818..75827
              /note="2.5 copies 4 mer TTAC 20% conserved"
repeat region 76136..76145
              /note="2.0 copies 5 mer TCATT 20% conserved"
repeat region 76515..76528
              /note="3.5 copies 4 mer CATT 28% conserved"
repeat region complement(76516..77245)
              /note="L2 repeat: matches 2448..3313 of consensus"
repeat region 77144..77153
              /note="2.5 copies 4 mer TGGA 20% conserved"
repeat region complement(77281..77325)
              /note="L2 repeat: matches 2304..2348 of consensus"
repeat region complement(77352..78690)
              /note="L2 repeat: matches 586..2082 of consensus"
repeat region 78727..78736
              /note="2.5 copies 4 mer TTTG 20% conserved"
repeat region 78739..78756
              /note="3.0 copies 6 mer GTTTTT 27% conserved"
repeat region complement(79263..79475)
              /note="MIR repeat: matches 10..241 of consensus"
repeat region 79532..79626
              /note="MIR repeat: matches 34..130 of consensus"
repeat region complement(79628..79686)
              /note="MLT1J1 repeat: matches 265..326 of consensus"
repeat region complement(79699..79732)
              /note="MLT1I repeat: matches 127..160 of consensus"
gene      complement(join(80437..80754,81615..81742))
          /gene="dJ1077I2.3"
mRNA      complement(join(80437..80754,81615..81742))
          /gene="dJ1077I2.3"
          /product="dJ1077I2.3 (Putative novel transcript)"
          /note="match: ESTs: Em:BF510052"
          /evidence=not_experimental
polyA site complement(80439)
          /gene="dJ1077I2.3"
repeat region 80508..80518
              /note="2.8 copies 4 mer ACAG 22% conserved"
repeat region 80761..80774
              /note="14.0 copies 1 mer A 28% conserved"
repeat region 81478..81489
              /note="3.0 copies 4 mer CTTC 24% conserved"
repeat region complement(81491..81658)
              /note="MLT1E repeat: matches 439..593 of consensus"
repeat region complement(81652..81945)
              /note="MLT1E repeat: matches 1..303 of consensus"
repeat region 82056..82073
              /note="3.6 copies 5 mer TTCAT 27% conserved"
repeat region 82067..82082
              /note="2.3 copies 7 mer TCATTTC 32% conserved"
repeat region 82072..82089
              /note="2.0 copies 9 mer TCTCATTTC 27% conserved"
repeat region 82359..82660

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| <u>repeat region</u> | /note="AluSx repeat: matches 1..297 of consensus" 82646..82660 |
| <u>repeat region</u> | /note="15.0 copies 1 mer A 30% conserved" complement(82983..83071) |
| <u>repeat region</u> | /note="MIR repeat: matches 47..144 of consensus" 83149..83158 |
| <u>repeat region</u> | /note="2.0 copies 5 mer CTTTT 20% conserved" 83257..83266 |
| <u>repeat region</u> | /note="10.0 copies 1 mer T 20% conserved" 83311..83325 |
| <u>repeat region</u> | /note="7.5 copies 2 mer AT 21% conserved" 83328..83621 |
| <u>repeat region</u> | /note="AluSq repeat: matches 2..299 of consensus" 83606..83615 |
| <u>repeat region</u> | /note="10.0 copies 1 mer A 20% conserved" 83891..83932 |
| <u>repeat region</u> | /note="21.0 copies 2 mer GT 84% conserved" 83931..83943 |
| <u>repeat region</u> | /note="3.2 copies 4 mer GTAG 26% conserved" 84233..84247 |
| <u>repeat region</u> | /note="7.5 copies 2 mer GT 21% conserved" 84562..84573 |
| <u>repeat region</u> | /note="2.0 copies 6 mer TATTCT 24% conserved" 85418..85429 |
| <u>repeat region</u> | /note="2.4 copies 5 mer GGTCA 24% conserved" 85511..85521 |
| <u>repeat region</u> | /note="2.2 copies 5 mer AAATA 22% conserved" 86153..86211 |
| <u>repeat region</u> | /note="11.8 copies 5 mer GTTTT 118% conserved" 86312..86322 |
| <u>repeat region</u> | /note="2.2 copies 5 mer TAATG 22% conserved" complement(86895..87015) |
| <u>repeat region</u> | /note="MER5B repeat: matches 54..172 of consensus" 87029..87150 |
| <u>repeat region</u> | /note="L2 repeat: matches 3144..3272 of consensus" 87464..87474 |
| <u>repeat region</u> | /note="2.8 copies 4 mer CCTC 22% conserved" 87614..87624 |
| <u>repeat region</u> | /note="2.2 copies 5 mer TTCCA 22% conserved" 87870..88316 |
| <u>misc feature</u> | /note="match: GSS: Em:AQ457776" |
| <u>repeat region</u> | 88004..88016 |
| <u>repeat region</u> | /note="2.2 copies 6 mer AGCTAG 26% conserved" 88039..88048 |
| <u>repeat region</u> | /note="2.5 copies 4 mer AGCA 20% conserved" 88332..88345 |
| <u>repeat region</u> | /note="3.5 copies 4 mer AAGC 28% conserved" 88590..88599 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TGAA 20% conserved" 88730..88741 |
| <u>repeat region</u> | /note="2.0 copies 6 mer AAAAGT 24% conserved" 88842..89139 |
| <u>repeat region</u> | /note="AluSx repeat: matches 1..293 of consensus" 88962..88978 |
| <u>repeat region</u> | /note="2.1 copies 8 mer AAAAATAC 34% conserved" 89129..89139 |
| <u>repeat region</u> | /note="11.0 copies 1 mer A 22% conserved" complement(89924..90101) |
| <u>repeat region</u> | /note="MER5A repeat: matches 6..189 of consensus" 90107..90117 |
| <u>repeat region</u> | /note="2.2 copies 5 mer AATTA 22% conserved" 90203..90214 |
| <u>repeat region</u> | /note="2.0 copies 6 mer TAAAAT 24% conserved" 90216..90227 |
| <u>repeat region</u> | /note="2.0 copies 6 mer ACACAT 24% conserved" |

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| <u>repeat region</u> | 90226..90239 |
| | /note="2.3 copies 6 mer ATCCAT 28% conserved" |
| <u>repeat region</u> | 90236..90251 |
| | /note="8.0 copies 2 mer AT 32% conserved" |
| <u>repeat region</u> | 90251..90261 |
| | /note="5.5 copies 2 mer TG 22% conserved" |
| <u>repeat region</u> | 90309..90630 |
| | /note="AluSx repeat: matches 1..307 of consensus" |
| <u>repeat region</u> | 90432..90452 |
| | /note="21.0 copies 1 mer A 42% conserved" |
| <u>repeat region</u> | 90608..90630 |
| | /note="5.8 copies 4 mer AAAT 46% conserved" |
| <u>repeat region</u> | 90655..90675 |
| | /note="10.5 copies 2 mer AT 24% conserved" |
| <u>repeat region</u> | 90658..90674 |
| | /note="2.8 copies 6 mer TATATT 34% conserved" |
| <u>repeat region</u> | 90678..90690 |
| | /note="2.2 copies 6 mer CATATA 26% conserved" |
| <u>repeat region</u> | 90794..90806 |
| | /note="2.2 copies 6 mer TCAGAA 26% conserved" |
| <u>repeat region</u> | 91258..91267 |
| | /note="2.5 copies 4 mer TTCC 20% conserved" |
| <u>repeat region</u> | complement(91289..91616) |
| | /note="L2 repeat: matches 2982..3312 of consensus" |
| <u>repeat region</u> | 91291..91300 |
| | /note="2.5 copies 4 mer CATT 20% conserved" |
| <u>repeat region</u> | 91549..91558 |
| | /note="5.0 copies 2 mer CT 20% conserved" |
| <u>repeat region</u> | 91758..91768 |
| | /note="5.5 copies 2 mer TG 22% conserved" |
| <u>repeat region</u> | 91819..91830 |
| | /note="2.4 copies 5 mer AAAAG 24% conserved" |
| <u>repeat region</u> | complement(91840..91994) |
| | /note="L2 repeat: matches 2945..3108 of consensus" |
| <u>repeat region</u> | complement(92094..92166) |
| | /note="MER91A repeat: matches 8..82 of consensus" |
| <u>repeat region</u> | 92259..92272 |
| | /note="3.5 copies 4 mer CATT 28% conserved" |
| <u>repeat region</u> | 92299..92309 |
| | /note="11.0 copies 1 mer T 22% conserved" |
| <u>repeat region</u> | 92487..92791 |
| | /note="AluSx repeat: matches 1..305 of consensus" |
| <u>repeat region</u> | 92695..92706 |
| | /note="2.0 copies 6 mer GGAGGT 24% conserved" |
| <u>repeat region</u> | 92769..92791 |
| | /note="23.0 copies 1 mer A 46% conserved" |
| <u>repeat region</u> | 92910..92927 |
| | /note="2.2 copies 8 mer GGGATCAT 36% conserved" |
| <u>repeat region</u> | 93142..93196 |
| | /note="MIR repeat: matches 113..163 of consensus" |
| <u>repeat region</u> | 93281..93298 |
| | /note="2.0 copies 9 mer AGGTGGAGG 36% conserved" |
| <u>repeat region</u> | 93288..93300 |
| | /note="2.2 copies 6 mer GGAGGT 26% conserved" |
| <u>repeat region</u> | 93398..93408 |
| | /note="2.2 copies 5 mer AGAGA 22% conserved" |
| <u>repeat region</u> | complement(93452..93501) |
| | /note="MIR repeat: matches 91..144 of consensus" |
| <u>repeat region</u> | 93557..93568 |
| | /note="2.4 copies 5 mer AAAAT 24% conserved" |
| <u>repeat region</u> | 93566..93577 |
| | /note="2.0 copies 6 mer TAACAG 24% conserved" |
| <u>repeat region</u> | 93606..93832 |
| | /note="AluSq repeat: matches 1..225 of consensus" |
| <u>repeat region</u> | 93751..93760 |

| | |
|----------------------|---|
| <u>repeat region</u> | /note="3.3 copies 3 mer GTG 20% conserved" 94085..94098 |
| <u>repeat region</u> | /note="14.0 copies 1 mer A 28% conserved" 94355..94452 |
| <u>repeat region</u> | /note="MIR repeat: matches 111..219 of consensus" 94503..94647 |
| <u>repeat region</u> | /note="LTR33 repeat: matches 14..160 of consensus" 94674..94898 |
| <u>repeat region</u> | /note="LTR33 repeat: matches 301..521 of consensus" 95374..95677 |
| <u>repeat region</u> | /note="AluSx repeat: matches 1..306 of consensus" 95654..95677 |
| <u>repeat region</u> | /note="24.0 copies 1 mer A 30% conserved" complement(95813..96278) |
| <u>repeat region</u> | /note="LTR37B repeat: matches 1..468 of consensus" 95893..95902 |
| <u>repeat region</u> | /note="2.5 copies 4 mer AATG 20% conserved" 95972..95981 |
| <u>repeat region</u> | /note="3.3 copies 3 mer ATG 20% conserved" 96295..96360 |
| <u>repeat region</u> | /note="L2 repeat: matches 3198..3268 of consensus" 96404..96415 |
| <u>repeat region</u> | /note="2.4 copies 5 mer AGCTA 24% conserved" 96976..96989 |
| <u>repeat region</u> | /note="14.0 copies 1 mer T 28% conserved" complement(97136..97231) |
| <u>repeat region</u> | /note="MLT1H repeat: matches 453..549 of consensus" complement(97339..97441) |
| <u>repeat region</u> | /note="MLT1H repeat: matches 197..305 of consensus" 97505..97822 |
| <u>misc feature</u> | /note="AluSq repeat: matches 1..307 of consensus" 97582..98164 |
| <u>repeat region</u> | /note="match: GSS: Em:AQ318861" 97649..97661 |
| <u>repeat region</u> | /note="4.3 copies 3 mer GTG 26% conserved" 97799..97819 |
| <u>repeat region</u> | /note="21.0 copies 1 mer A 33% conserved" complement(97917..98012) |
| <u>repeat region</u> | /note="MIR repeat: matches 17..113 of consensus" 97968..97983 |
| <u>repeat region</u> | /note="2.7 copies 6 mer GACCCA 32% conserved" 98280..98295 |
| <u>repeat region</u> | /note="2.7 copies 6 mer GCCTGG 23% conserved" 98622..98640 |
| <u>repeat region</u> | /note="1.9 copies 10 mer CTGGTGGCCA 38% conserved" 98636..98646 |
| <u>repeat region</u> | /note="2.2 copies 5 mer TGGCC 22% conserved" 98827..98849 |
| <u>misc feature</u> | /note="23.0 copies 1 mer T 28% conserved" complement(98879..99267) |
| <u>misc feature</u> | /note="match: GSS: Em:AQ630216" 99384..99798 |
| <u>repeat region</u> | /note="match: GSS: Em:AQ718436" 99746..99755 |
| <u>repeat region</u> | /note="2.5 copies 4 mer TCCA 20% conserved" 100252..100265 |
| <u>repeat region</u> | /note="2.0 copies 7 mer TGTGTGT 28% conserved" 100409..100419 |
| <u>repeat region</u> | /note="2.2 copies 5 mer TAAAA 22% conserved" 100973..100999 |
| <u>repeat region</u> | /note="3.0 copies 9 mer ACTCTGACC 36% conserved" 101677..101688 |
| <u>repeat region</u> | /note="3.0 copies 4 mer CTTT 24% conserved" complement(101824..102026) |
| <u>repeat region</u> | /note="L1MC4 repeat: matches 6797..7002 of consensus" |

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/note="MADE1 repeat: matches 1..53 of consensus"
repeat region 102189..102204
/note="2.7 copies 6 mer TTAACA 23% conserved"
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/note="MLT1J repeat: matches 1..421 of consensus"
misc feature complement(102530..103055)
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repeat region 103849..103861
/note="2.6 copies 5 mer CAACC 26% conserved"
repeat region 104032..104047
/note="4.0 copies 4 mer ATCA 32% conserved"
repeat region 104165..104175
/note="2.2 copies 5 mer GGAAA 22% conserved"
repeat region 104471..104777
/note="153.5 copies 2 mer CT 150% conserved"
repeat region 104488..104776
/note="57.8 copies 5 mer TCTTC 240% conserved"
repeat region 104660..104720
/note="20.3 copies 3 mer TTC 37% conserved"
repeat region 105141..105293
/note="FRAM repeat: matches 1..153 of consensus"
repeat region 105849..106273
/note="L2 repeat: matches 2828..3273 of consensus"
repeat region 106110..106128
/note="6.3 copies 3 mer TCT 22% conserved"
repeat region 106112..106121
/note="2.5 copies 4 mer TTCT 20% conserved"
repeat region 106115..106125
/note="2.2 copies 5 mer TTTCT 22% conserved"
repeat region 106145..106155
/note="2.2 copies 5 mer TGATC 22% conserved"
repeat region 106155..106166
/note="3.0 copies 4 mer TTAT 24% conserved"
repeat region 106283..106347
/note="16.2 copies 4 mer TGGA 78% conserved"
repeat region 106375..106397
/note="1.9 copies 12 mer AGACAAATGGAC 46% conserved"
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